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DISEASE NOTES

First Report of a Leaf Spot Caused by *Boeremia exigua* var. *exigua* on *Hydrangea paniculata* in Italy

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Panicle hydrangea (*Hydrangea paniculata*) is a perennial ornamental plant belonging to the Saxifragaceae commonly used in gardens, characterized by massive upright flowers from midsummer to autumn. Starting from the end of August 2017, a previously unknown leaf spot was observed on 2- to 3-year-old plants of *H. paniculata* grown in borders in a garden located in Valle Cervo near Biella, northern Italy (45°36′00″N, 8°03′00″E). Ten out of 20 plants grown in this garden were affected, with 30 to 40% of leaves showing symptoms, consisting initially of circular necrotic spots, with diameter ranging between 20 and 80 mm, well defined by a brown margin. Severely infected leaves became chlorotic and abscised. The disease started from basal leaves on plants grown in shadow, at high relative humidity. In several isolations carried out from infected tissues on potato dextrose agar amended with 25 mg/liter of streptomycin sulfate a fungus was consistently isolated. After 15 days of incubation, black pycnidia, 127 to 255 µm diameter, developed, releasing hyaline, elliptical, nonseptate conidia, measuring 4.3 to 10.3 µm (average 6.9 µm) × 1.9 to 4.1 µm (average 2.7 µm). On the basis of its morphological characteristics, the fungus was identified as *Phoma* sp. (Boerema et al. 1976). The internal transcribed spacer (ITS) region of rDNA was amplified using the primers ITS1/ITS4 and sequenced. BLAST analysis of the 517 bp obtained showed 100% homology with *Boeremia exigua* (formerly *Phoma exigua*) (GenBank accession nos. MF039478, MF599109, and MF599108). The nucleotide sequence has been assigned the GenBank accession number MG766873. Because ITS analysis was not able to identify the varietas of this species, additional genes (elongation factor 1 alpha gene [EF1α] and β-tubulin [BTUB]) were amplified with primers EF1-728F/EF2 and Bt2a/Bt2b, respectively, and sequenced. BLAST analysis of the EF1α 449-bp sequence (GenBank accession no. MG970366) and the BTUB 372-bp sequence (GenBank accession no. MG970365) showed 100 and 99% similarity with the sequences of *B. exigua*var. *exigua* (GenBank accession nos. KY550228 and KR010463, respectively). Pathogenicity tests were performed by spraying leaves of healthy 24-month-old *H. paniculata* plants grown in pots at temperatures between 16 and 22°C with a spore and mycelial suspension (10^6 CFU/ml). After artificial inoculation, leaves were covered with transparent plastic bags for 5 days. Plants sprayed only with sterile water served as a control. Three plants were used for each treatment. Lesions similar to those seen in naturally infected

leaves developed on leaves 7 to 10 days after inoculation in all three inoculated plants, whereas control plants remained healthy. The same fungus was consistently reisolated from the lesions. The pathogenicity test was carried out twice. To our knowledge, this is the first report of *B. exigua* var. *exigua* on *H. paniculata* in Italy. The pathogen has been previously reported on *H. macrophylla* in Italy and the United States (Farr and Rossman 2017; Garibaldi et al. 2006). The disease is at present limited to a few gardens in the mountain region where it was observed.

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